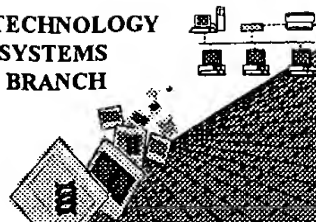# RAW SEQUENCE LISTING ERROR REPORT

RECEIVED MAR 0 4 2002 TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: **09/922,067ß**

Source: **OIPE**

Date Processed by STIC: **2/11/2002**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO **REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
         Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

SERIAL NUMBER: _09/922,067B_

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _5-7_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,067B

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02112002\I922067B.raw

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 4 <110> APPLICANT: MacPhee, Colin Houston
 5         Tew, David Graham
 6         Southan, Christopher Donald
 7         Hickey, Deirdre Mary Bernadette
 8         Gloger, Israel Simon
 9         Lawrence, Geoffrey Mark Prouse
10         Rice, Simon Quentyn John
12 <120> TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2,
13         Inhibitors Thereof and Use of the Same in Diagnosis and
14         Therapy
16 <130> FILE REFERENCE: P30693C4X1C1
18 <140> CURRENT APPLICATION NUMBER: US/09/922,067B
19 <141> CURRENT FILING DATE: 2001-08-03
21 <150> PRIOR APPLICATION NUMBER: 09/193,130
22 <151> PRIOR FILING DATE: 2000-11-28
24 <150> PRIOR APPLICATION NUMBER: 08/387,858
25 <151> PRIOR FILING DATE: 1994-06-24
27 <150> PRIOR APPLICATION NUMBER: PCT/GB94/01374
28 <151> PRIOR FILING DATE: 1994-06-24
30 <150> PRIOR APPLICATION NUMBER: GB 9313144.9
31 <151> PRIOR FILING DATE: 1993-06-25
33 <160> NUMBER OF SEQ ID NOS: 11
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 37
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapien
42 <400> SEQUENCE: 1
43 Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
44  1               5                  10                  15
45 Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
46            20                  25                  30
47 Lys Asp Phe Asp Gln
48          35
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 30
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapien
56 <400> SEQUENCE: 2
57 Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
58  1               5                  10                  15
59 Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
60            20                  25                  30
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,067B

DATE: 02/11/2002
TIME: 12:59:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02112002\I922067B.raw

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63  <210> SEQ ID NO: 3
64  <211> LENGTH: 27
65  <212> TYPE: PRT
66  <213> ORGANISM: Homo sapien
68  <400> SEQUENCE: 3
69  Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
70  1               5                   10                  15
71  Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
72              20                  25

75  <210> SEQ ID NO: 4
76  <211> LENGTH: 19
77  <212> TYPE: PRT
78  <213> ORGANISM: Homo sapien
80  <400> SEQUENCE: 4
81  Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
82  1               5                   10                  15
83  Pro Ala Asn

87  <210> SEQ ID NO: 5
88  <211> LENGTH: 420
89  <212> TYPE: DNA
90  <213> ORGANISM: Unknown    see item 11 on Eva Summary sheet
92  <220> FEATURE:
93  <223> OTHER INFORMATION: Where N can be represented by A, C, T, or G
95  <221> NAME/KEY: misc_feature
96  <222> LOCATION: 265, 390, 395, 403, 406
97  <223> OTHER INFORMATION: n = A,T,C or G
99  <400> SEQUENCE: 5
100 aaaaaaccta ttttaatcct aattgtattt ctctattcct gaagagttct gtaacatgat 60
101 gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctccttcaat 120
102 caagcagtcc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180
103 tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240
104 catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300
105 acccctgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcattttat 360
106 gatattagca ggatattgga aatattcagn gttgntaaaa agnggnggct gagggattct 420

109 <210> SEQ ID NO: 6
110 <211> LENGTH: 379
111 <212> TYPE: DNA
112 <213> ORGANISM: Unknown    item 11
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Where N can be represented by A, C, T, or G
117 <221> NAME/KEY: misc_feature
118 <222> LOCATION: 84
119 <223> OTHER INFORMATION: n = A,T,C or G
121 <400> SEQUENCE: 6
122 tgctaatatc ataaaaatga aaaatgcta ctcacctgat aaagaaagaa agatgattac 60
123 aatcaggggt tcagtccacc agantttttgc tgacttcact tttgcaactg gcaaaataat 120
124 tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
125 caaagcttca ttagcattct tacaaaagca tttaggactt cataaagatt ttgttcagtg 240
126 ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
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RAW SEQUENCE LISTING   DATE: 02/11/2002
PATENT APPLICATION: US/09/922,067B   TIME: 12:59:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02112002\I922067B.raw

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127 caattcaaca catcatgttt acagaacttc ttccagggaa taggaggaaa tacaattggg 360
128 gtttaaaata ggtttttttt                                            379
130 <210> SEQ ID NO: 7
131 <211> LENGTH: 279
132 <212> TYPE: DNA
133 <213> ORGANISM: (Unknown)  ıtem 11
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Where N can be represented by A, C, T, or G
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: 257
140 <223> OTHER INFORMATION: n = A,T,C or G
142 <400> SEQUENCE: 7
143 gaagaatgca ttagatttaa agtttgatat ggaacaactg aaggactcta ttgataggga 60
144 aaaaatagca gtaattggac attcttttgg tggagcaacg gttattcaga ctcttagtga 120
145 agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
146 agtatattcc agaattcctc agcccctctt ttttatcaac tctgaatatt tccaatatcc 240
147 tgctaatatc ataaaantgg aaaaatgcta ctcacctgg                       279
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 572
151 <212> TYPE: DNA
152 <213> ORGANISM: Homo sapien
154 <400> SEQUENCE: 8
155 aaaatagcag taattggaca ttctttaggt ggagcaacgg ttattcagac tcttagtgaa 60
156 gatcagagat tcagatgtgg tattgccctg gatgcatgga tgtttccact gggtgatgaa 120
157 gtatattcca gaattcctca gcccctcttt tttatcaact ctgaatattt ccaatatcct 180
158 gctaatatca taaaaatgaa aaaatgctac tcacctgata agaaagaaa gatgattaca 240
159 atcaggggtt cagtccacca gaattttgct gacttcactt ttgcaactgg caaaataatt 300
160 ggacacatgc tcaaattaaa gggagacata gattcaaatg tagctattga tcttagcaac 360
161 aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
162 gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
163 aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540
164 aggtttttta aaaaaaaaaa aaaaaaaact cg                               572
166 <210> SEQ ID NO: 9
167 <211> LENGTH: 1361
168 <212> TYPE: DNA
169 <213> ORGANISM: Homo sapien
171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (38)...(1360)
175 <400> SEQUENCE: 9
176 tgagagacta agctgaaact gctgctcagc tcccaag atg gtg cca ccc aaa ttg  55
177                                            Met Val Pro Pro Lys Leu
178                                             1               5
180 cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt 103
181 His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
182              10              15              20
184 gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg 151
185 Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
186          25              30              35
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/922,067B

DATE: 02/11/2002
TIME: 12:59:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02112002\I922067B.raw

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188 gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act   199
189 Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
190     40              45                  50
192 aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgt aca gac tta   247
193 Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
194 55              60                  65                  70
196 atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca   295
197 Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
198             75                  80                  85
200 tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa   343
201 Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
202             90                  95                  100
204 tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc   391
205 Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly
206             105                 110                 115
208 aac att ttg agg tta ctc ttt ggt tca atg aca act cct gca aac tgg   439
209 Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp
210     120                 125                 130
212 aat tcc cct ctg agg cct ggt gaa aaa tat cca ctt gtt gtt ttt tct   487
213 Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser
214 135             140                 145                 150
216 cat ggt ctt ggg gca ttc agg aca ctt tat tct gct att ggc att gac   535
217 His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp
218             155                 160                 165
220 ctg gca tct cat ggg ttt ata gtt gct gct gta gaa cac aga gat aga   583
221 Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg
222             170                 175                 180
224 tct gca tct gca act tac tat ttc aag gac caa tct gct gca gaa ata   631
225 Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile
226.            185                 190                 195
228 ggg gac aag tct tgg ctc tac ctt aga acc ctg aaa caa gag gag gag   679
229 Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu
230     200                 205                 210
232 aca cat ata cga aat gag cag gta cgg caa aga gca aaa gaa tgt tcc   727
233 Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser
234 215                 220                 225                 230
236 caa gct ctc agt ctg att ctt gac att gat cat gga aag cca gtg aag   775
237 Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys
238             235                 240                 245
240 aat gca tta gat tta aag ttt gat atg gaa caa ctg aag gac tct att   823
241 Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile
242             250                 255                 260
244 gat agg gaa aaa ata gca gta att gga cat tct ttt ggt gga gca acg   871
245 Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr
246             265                 270                 275
248 gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc   919
249 Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala
250     280                 285                 290
252 ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att   967
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2/11/02

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253 Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile
254 295             300             305             310
256 cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct      1015
257 Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala
258             315             320             325
260 aat atc ata aaa atg aaa aaa tgc tac tca cct gat aaa gaa aga aag      1063
261 Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys
262             330             335             340
264 atg att aca atc agg ggt tca gtc cac cag aat ttt gct gac ttc act      1111
265 Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
266         345             350             355
268 ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac      1159
269 Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp
270         360             365             370
272 ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca      1207
273 Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala
274 375             380             385             390
276 ttc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac      1255
277 Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp
278             395             400             405
280 tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att      1303
281 Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile
282             410             415             420
284 aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag      1351
285 Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu
286         425             430 .           435
288 aaa tac aat t                                                        1361
289 Lys Tyr Asn
290     440
293 <210> SEQ ID NO: 10
294 <211> LENGTH: 7
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapien
298 <400> SEQUENCE: 10
299 Gln Tyr Ile Asn Pro Val Ala
300 1               5
303 <210> SEQ ID NO: 11
304 <211> LENGTH: 20
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapien
308 <400> SEQUENCE: 11
309 Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
310 1               5               10              15
311 Phe Ala Thr Gly
312             20
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VERIFICATION SUMMARY   DATE: 02/11/2002
PATENT APPLICATION: US/09/922,067B   TIME: 12:59:48

        Input Set : A:\seqlist.txt
        Output Set: N:\CRF3\02112002\I922067B.raw

L:18 M:270 C: Current Application Number differs, Wrong Format
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7